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Copyright (c) 1993 - 2000 Compugen Ltd
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ALIGNMENTS

W62828 standard; Protein; 666 AA.

PN XX PPR XX PR XX N-PSDB; V42310. WPI; 1998-377279/32 02-JUL-1998 Bower NI, Goulter KC, WO9827805-A1. Protein кеу Macadamia integrifolia. antimicrobial protein; infestation; control. Macadamia integrifolia antimicrobial protein. 27-OCT-1998 (first entry) 20-DEC-1996; 22-DEC-1997; Peptide (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY 96AU-0004275 97WO-AU00874 /note= "signal peptide" 29..666 /note= "mature protein" Location/Qualifiers Green JL, Manners JM, Marcus JP;

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                                        KEEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRY
                                                                                                                                                                                                                                                                             DPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERM
                                                                                                                                                                                                                                                                                                                                 KRFEEDIDWSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEEYNRQR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 43-45; 96pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or man % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right
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Recombinant cocoa proteins - are responsible beans and produced in large quantities using
                                                                                                                                                                Cocoa; flavour;
                                                                                                                                                                                                                                R20181 standard;
                          N-PSDB;
                                                                                                 07-JUN-1991;
                                                                                                                  26-DEC-1991
                                                                                                                                 W09119801-A
                                                                                                                                                  Theobroma cacao
                                                                                                                                                                               Sequence encoded by 67 kD T.
                                                                (MRSC ) MARS
                                                                                 11-JUN-1990;
                                                                                                                                                                                                16-APR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       462
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                        1992-024418/03.
DB; Q20377.
                                                                                                                                                                                                                                                                       LFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPGPR
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                                                Hodge R,
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                                                                                                  91WO-GB00914
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                                                                                                                                                                                                                                Protein;
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                                                                                                                                                                               cacao protein cDNA.
                                                  ΕA,
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Best Local
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             antimicrobial protein;
                                         Gossypium hirsutum antimicrobial protein.
                                                                        27-OCT-1998
                                                                                                                                  W62832 standard; Protein; 590 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologies between the 67 kD polypeptide and the vicilins, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICEEEEEYNR---QRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRY 165
                                                                                                                                                                                                    ifnnpdesyfmsfsqqrqr---rderrgnplasildf
                                                                                                                                                                                                                                                                                   GHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEE
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                                                                                                                                                                                                                                        SFNSQDQSIFFPGPRQHQQQSPRSTKQQQPLVSILDF 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vpagstvyvvsqdnqekltiavlalpvnspgkyelffpagnnkpesyygafsyevletvf
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                                                                                                                                                                                                                                                                  ghavtffaskdqplnavafglnaqnnqriflagk-knlvrqmdseakelsfgvpsklvdn
                                                                                                                                                                                                                                                                                                                               tdgygyaqmacphlsrqsqgsqsgrqdrreqeeeseeetfgefqqvkaplspgdvfvapa
                                                                                                                                                                                                                                                                                                                                                            ASGEADVEMACPHLSGRHGGRGGGK--RHEEEEDV-----HYEQVRARLSKREAIVVLA
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                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.8%; Score 1127; DB 13; 40.4%; Pred. No. 1.4e-89;
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             infestation; control
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Matches 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of an antimicrobial protein which can
be used to control microbial infestations in plants and man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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les 235; Conser
                                                                              YRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRGGG
                                                                                                                                                                                                                                                    hr pvnnpg q feeft pags qrpq sylrafsreile pafntr seql del f g grqs rrrqq g q
                                                                                                                                                                                                                                                                       LQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFG-------QQRE 418
RQHQQQS 647
                         glyngninpdhngrifvagkinhv-rqwdsqakelafgvssrlvdeifnsnpqesyfvs-
                                                   G-----INAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPGP
                                                                                                           KRHEEEEDV------HYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAF 585
                                                                                                                                                                                                                           GVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED 478
                                                                                                                                                                                                                                                                                                             hcdaekiylvtngrgtltflthenkesynivpgvvvKvpagstvylanqdnkekliiavl 295
                                                                                                                                                                                                                                                                                                                                           HLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF
                                                                                                                                                                                                                                                                                                                                                                                      EQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT 305
                                                                                                                                                                                                                                                                                                                                                                                                                            fqecqqhchqqeqrpekkqqcvrecrekyqe.....npwrgereeeaeeeeteegeq
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEDCRRRCEQQE--PRQQHQCQLRCREQQRQHGRGGDMMNPQRG-----GSGRYEEGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --rqqeerqqpqcqqrclkrfeqeqqq------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQRE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \tt ddppkryedcrrrcewdtrgqkeqqqceescksqygekdqqqrhrpedpqrryeecqqec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQYEQCQKHC 133
                                                                                                                                       frqlrdinvtvsalqlnqgsifvphynskatfvilvtegngyaemvsphlp----rqss
                                                                                                                                                                                               gmfrkasqeqiralsqeatspr----eksge--rfafnllsqtprysnqngrffeacppe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-microbial protein from e.g. Macadamia integrifolia -
l for controlling microbial infestations of plants or mammals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 49-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.2%; Score 1103.5; ilarity 38.7%; Pred. No. 1.7e Conservative 110; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96AU-0004275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-AU00874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manners JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5; DB 19;
1.7e-87;
nes 175; Ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marcus JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---sqrq 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                       355
                                                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                409
                                                                                                                                                                                                                                                                                                                                            365
                                                                                                                                                                                                                                                                                                                                                                       235
                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
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                                                                                                                                                                                                                                                                  RESULT
W62831
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                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                         Matches 210;
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                        The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                   Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or mar
                                                                                                                                                                                                                                                                                                                  Claim 1; Page 47-49; 96pp; English
                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-377279/32
                                                                                                                                                                                                                                                                                                                                                                              Bower NI,
                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9827805-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theobroma cacao.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antimicrobial protein; infestation; control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theobroma cacao antimicrobial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W62831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W62831 standard;
                                                                                                                                                                                   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
455 YNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVV 514
                                                                                    176
                                                                                                                     117
                                                                                                                                                                    166 EEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQHQCQLRCREQQRQH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71
                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                           LRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIR 342
                                                                                                                           GRGGDMMNPQRGGSGRYEEGEEEQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKL 282
                                                                                                                                                  keqqrqqeeel------qrqyqqcqgrcqeqqqggreqqqcqrkcweqykeq 116
                                 NTQTEKLRGVFGQQR-----EGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGP 454
                                               IPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAAL 402
                                                                                                                   ntqrekleeileeqrgqkrqqgqqgmfrkakpeqiraisqqatsprh----rgge--rla
                                                                                  lkgindyrlamfeanpntfilphhcdaeaiyfvtngkgtitfvthenkesynvgrgtvvs
                                                                                                                                                                                                                                                                                                                                                                              Goulter KC,
                                                                                                                                                                                                                                                                  525
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589
                                                                                                                                                                                                                                                                                                                                                                                                               96AU-0004275
                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-AU00874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                               28.9%;
                                                                                                                                                                                                                                                                                                                                                                            Green JL,
                                                                                                                                                                                                                       Score 1025; DB 19;
Pred. No. 9.3e-81;
Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                             Manners JM,
                                                                                                                                                                                                                                                                                                                                                                             Marcus
                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                       Indels 54;
                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                   can
                                                                                                                                                                                                                                                                                           mammalian
                                                                                                                                                                                                                                                                                                                                   or mammals
                                                                                                                                                                                                                                         525;
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       11;
Q
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Best Local Similarity
Matches 197; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 58-60; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bower NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial protein; infestation; control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W62835 standard; Protein; 593 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays antimicrobial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 GHPVVFVSSGNENLLLFAFGINAQNNHENFLAGR 600
                                                                                                                                                                                                                                                                                                        25 eddnhhhhgghksgqcvrrcedrpwhqrprcleqcreeerekrqersrheaddrsgegss 84
                                                                NNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQ 415
                                    \tt grkklvitkilhtisvpgefqfffgpggrnpesflssfsksiqraayktssdrlerlfgr
                                                                                                                                                       ANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRD 355
                                                                                                                                                                                                                 edereqekekqkdrrpyvfdrrsfrrvvrseqgslrvlrpfdevsrllrgirdyrvavle 144
                                                                                                                                                                                                                                          ---RYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLE 295
--QREGVIIRASQEQIRELTRDDSE----SRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQ 470
                                                                                                                              anprsfvvpshtdahcicyvaegegvvttiengerrsytikqghvfvapagavtylantd 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tdgygyaqmacphlsrqsqgsqsgrqdrreqeeeseeetfgefqqvkaplspgdvfvapa 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASGEADVEMACPHLSGRHGGRGGGK--RHEEEEEDV-----HYEQVRARLSKREAIVVLA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goulter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96AU-0004275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-AU00874
                                                                                                                                                                                                                                                                                                                                                                                             25.4%; Score 898; DB 19; 39.2%; Pred. No. 1.2e-69; Vative 91; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Green JL, Manners JM,
                                                                                                                                                                                                                                                                                                                                                                                                  184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marcus
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mammalian
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                      238
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RESULT
W62837
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Best Local Similarity 35.1
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of an antimicrobial protein which \boldsymbol{\alpha} be used to control microbial infestations in plants and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antimicrobial protein; infestation; control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W62837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W62837 standard; Protein; 637
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel anti-microbial protein from e.g. Macadamia useful for controlling microbial infestations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare antimicrobial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 60-62; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bower NI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
    188 DPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRG----GDMMNPQRGGSGRYEEG
                                                                                           128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 lpgpeesggheeregeeeeree 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               531
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                                                                                                                                                          SKYDNQEDPQ--TECOQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEEYNRQRDPQQQYE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dsnlqivcfevhadrnekvflagad-nvlqkldrvakalsfaskaeevdevlgsrrekgf 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKR 187
                                                                                                                                   ashddeddrrgghslqqcvqrcrqer--pr---ysharcvqec-----rddqqqh- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHG----GRGGGKRHEEEEDVH------YEQVRARLSKREAIVVLAGHPVVFVSSG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPGPRQ---HQQQSPRSTKQQQ 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 yeadars fhdlaehdvs vs fan it agsm saplfn trsfki a yvpngkgyaeivcphr gsner and trsfki a yvpngkgyaeivcphr gsner a yvpngkgyaeivcphr gyngkgyaeivcphr gsner a yvpngkgyaeivcphr gsner a yvpngkgyaeivchr 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goulter KC,
                                                                                                                                                                                                                                                                                                                                 637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                              ---grheqeeeggrgrgwhgegereeehgrgrgrhgegereeehgrgrgrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96AU-0004275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-AU00874
                                                                                                                                                                                                                      24.4%; Score 864.5; DB 19; 35.1%; Pred. No. 1.1e-66; tive 98; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manners JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     integrifolia plants or man
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                              Length 637;
                                                                                                                                                                                                                                                                                                                                                                                            can
d mammalian
                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammals
                                                                                                                                                                                                                      Gaps
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      243
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                                                                                                                                                                                                                                        31-JAN-1998;
13-FEB-1998;
13-FEB-1998;
13-FEB-1998;
                                            WPI; 1999-479189/40.
N-PSDB; Z06382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergy; immune response; transgenic; allergen;
immunoglobulin E; Ig E; binding site; peanut.
                                                                                                                                                   (SOSI/) SOSIN H.
(UYAR-) UNIV ARKANSAS
(UYNY) UNIV NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arachis hypogea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y15244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y15244 standard; Protein; 626 AA
  Modified allergen with
                                                                                                             Bannon GA,
                                                                                                                                                                                                                                                                                                                               27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                          29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9938978-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peanut allergen, Ara h 1, amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EESFNSQDQSI-FFPGPRQHQQQSPRSTKQQQ 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHPVVFVSS--GNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E--EEQSDN--PYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gegereeergrghgrhgege-----reeergrgrgrhgegereeeegrgrgrrgeg
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                                                                                                             Burks AW,
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98US-0073283.
98US-0074590.
98US-0074624.
98US-0074633.
                                                                                                                                                                                                                                                                                                                                                                          99WO-US02031
                                                                                                                                                        MT SINAI SCHOOL MEDICINE
reduced IgE binding, useful for treating
                                                                                                             Sampson
                                                                                                             HA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sosin
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e.g.
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Best Local Similarity
Matches 212; Conserv
                30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By modifying the IgE binding sites the ability of the allergen to provoke an immune response is downregulated. The epitopes of the IgE binding sites can therefore be modified in genetically engineered plants and animals to elicit less of an allergic response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of the Ara h 1 protein from Arachis hypogea. The Ara h 1 protein has 23 IgE (1mmunoglobulin E) binding epitopes, four of which are immunodominant (Y15247, Y15249, Y15250).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --edwrrpshqq-pr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQTCQQRC---ERR----YEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQR 192
                                                                                                                                                              rpqsqsqspsspekesp
                                                                                                                                                                                                                        ll--gfginaennhriflagdkdnvidqiekqakdlafpgsgeqvekliknqkeshfvsa
                                                                                                                                                                                                                                                          LLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPG
                                                                                                                                                                                                                                                                                        rkeqqqrgr---reeeededeeeegsnrevrrytarlkegdvfimpaahpvainasselh
                                                                                                                                                                                                                                                                                                         HLSGRHGGRGGGKRHEEEEDVHYE----QVR----ARLSKREAIVVLAGHPVVFVSSGNEN
                                                                                                                                                                                                                                                                                                                                                        fgklfevkpdkknpglgdldmmltcveikegalmlphfnskamvivvvnkgtgnlelvav 470
                                                                                                                                                                                                                                                                                                                                                                                      YGQAYEVKPEDYR-QLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACP
                                                                                                                                                                                                                                                                                                                                                                                                                     rssennegvivkvskehveeltkhaks----vskkgseeegditnpinlregepdlsnn 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRG----PYNLFNKRPLYSNK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \verb|gqfedffpassrdqssylqgfsrntleaafnaefneirrvlleenaggeqeergqrrwst|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF------GQQR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQSDNPY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ksspyqkktenpcaqrclqscqqepddlkqk----acesrctkleydprcvydprgh
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                                                                               standard;
                                                                                                                                                                                                                                           626 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 108; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 35-37; 46pp; English
                (first entry)
                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----kirpegrege---
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Pred. No. 2.2e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -qewgtpgshvreetsrnnpf 175
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Best Local Similarity
Matches 212; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 desensitising patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chiromidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents a peanut (Arachis hypogea) allergen 1168391 Ara h I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting; chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee; screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat; cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig; mice; gerbil; vaccine; treatment; prevention; hypersensitivity; peanut.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-1998;
09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 70-71; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desensitizing patients to polypeptide allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999
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                  313
                                                                                                                                     134
                                                                                                                                                                           193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Major histocompatibility complex; class II; desensitising; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peanut allergen 1168391 Ara h I protein fragment.
                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                 93
LLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTISTP
                                                                        YFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAI
                                                                                                                                                                                                                                                                                                                               ESGPRQQQY---CQRRCKEICEEEEEYNRQRDPQQQYEQCQKHCQRRETEPR-----H 142
                                                    yfpsrrfstrygngngrirvlgrfdgrsrqfqnlgnhrivgieakpntlvlpkhadadni
                                                                                                                                 --edwrrpshqq-pr-----kirpegrege----qewgtpgshvreetsrnnpf
                                                                                                                                                                     EYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQSDNPY
                                                                                                                                                                                                            tgttnqrsppgertrgrqpgdydddrr--qprreeggrwgpagprerereed-wrqpr--
                                                                                                                                                                                                                                                    MQTCQQRC---ERR----YEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQR 192
                                                                                                                                                                                                                                                                                         ksspygkktenpcagrclqscqqepddlkqk-----acesrctkleydprcvydprgh 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Larche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 AA;
                                                                                                                                                                                                                                                                                                                                                                       Conservative 108;
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98GB-0000445
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                                                                                                                                                                                                                                                                                                                                                                   24:0%; Score 849.5;
34.4%; Pred. No. 2.26
tive 108; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 2.2e-65;
hes 204;
                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
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                                                                                                                                                                                                                                                                                                                                                                     93;
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RESULT
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This polypeptide comprises major peanut allergen Ara hI (W22149) Its sequence was deduced from cDNA clone P17 (T76612), isolated
                                                                      Claim 31; Page 169; 354pp; English
                                                                                                                         Peanut allergens Ara hI and A two-site monoclonal antibody
                                                                                                                                                                                                   WPI; 1997-363453/33
N-PSDB; T76612.
                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1996;
29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody; ELISA; analysis; Ara hI.
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27-OCT-1998

(first entry)

W62834 standard; Peptide;

614 B

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Best Local Similarity
Matches 219; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see w24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site MAB ELISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara hI antigen epitopes (see W24165-87) may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock.
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                                     G-PRQHQQQSPRSTKQQQ------PLVSIL 661
                                                                                                           NLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFP
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                        NLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFP 638
                                                                    vrkeqqqrgrreqeweeeeedeeegsnrevrrytarlkegdvfimpaahpvainassel
                                                                                                            PHLSGRHGGRGGGKRHEEEEEDVHYE----QVR---ARLSKREAIVVLAGHPVVFVSSGNE
                                                                                                                                                                                                                                                                                       R------EGVIIRASOEQIRELTRDDSESRHWHIRRGGESS--RGPYNLFNKRPLYSN 466
                                                                                                                                                                                                                                                                                                                                                       vntpggfedffpassrdgssylggfsrntleaafnaefneirrvlleenaggegeerggr 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTEYLINRDNNERLHIAKFLQT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nnpfyfpsrrfstrygnqngrirvlqrfdqrskqfqnlqnhrivqiearpntlvlpkhad\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pr----edwrrpshqq-pr------kirpegrege----qewgtpgsevreetsr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COKHCORRETEPRHMOTCOORCERRYEKEKRKOOKRYEEQOREDEEKYEERMKEEDNKRD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKYDNQEDPQTEC-QQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQRDPQQQYEQ 128
                                                                                                                                                             nfgrlfevkpdkknpqlqdldmmltcveikegalmlphfnskamvivvvnkgtgnlelva
                                                                                                                                                                                                              KYGQAYEVKPEDYR-QLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMAC
                                                                                                                                                                                                                                                          rrstrssdnegvivkvskehvqeltkhaksvs----kkgseeeditnpinlrdgepdlsn
                                                                                                                                                                                                                                                                                                                                                                                                   ISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF------GQQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                adnilviqqgqatvtvangnnrksfnldeghalripsgfisyilnrhdnqnlrvakismp 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POOREYEDCRRRCEQQEPROQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----tgatnqrhppgertrgrqpgdydddrrqprreeggrwgpaeprerereed-wrq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spyrktenp---caqrclqsc-qqepddlkqkacesrctkl----ey---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 55-57; 96pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goulter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.0%; Score 849; DB 19; ilarity 34.7%; Pred. No. 2.3e-65; Conservative 110; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96AU-0004275
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Green JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manners JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marcus JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 614;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                  461
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Query Match Best Local Similarity

23.8%; Score 843.5; D 34.2%; Pred. No. 7.2e-

DB 18;

Length 626;

211;

Conservative

108;

Mismatches

Indels

93;

Gaps

20;

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W22150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
                                   This polypeptide comprises major peanut allergen Ara hI (W22149). Its sequence was deduced from cDNA clone P41b (T76613), isolated from peanut seed cDNA using a primer (see T76616) based on an isolated Ara hI peptide (see W24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The allergen is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hI and Ara hII (see W24164) can be used to raise monoclonal antibodies which are used in a specific two-site MAD ELISA for the detection of Ara hI ara hI (claimed). IgE-binding Ara hI antigen epitopes (see W24165-87) may be used in vaccines to protect against allergic reactions to peanut allergens
                                                                                                                                                                                                                         Claim 31; Page 172; 354pp; English.
                                                                                                                                                                                                                                                     Peanut allergens Ara hI and Ara hII - used two-site monoclonal antibody based ELISA
                                                                                                                                                                                                                                                                                                                                        Bannon GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arachis hypogaea strain Florunner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monoclonal antibody; ELISA; analysis; Ara hI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W22150 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUL-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peanut allergen Ara hI.
                                                                                                                                                                                                                                                                                                                                                                    (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 G-PRQHQQQSPRSTKQQQ-----PLVSIL 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 arpqsqspsspekedqeeenqggkgpllsil 610
                           anaphylactic shock.
                                                                                                                                                                                                                                                                                               1997-363453/33.
DB; T76613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hll--gfginaennhriflagdkdnvidqiekqakdlafpgsgeqvekliknqreshfvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seed storage protein; allergen; allergy; hypersensitivity;
; anaphylactic shock; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                        Burks AW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              96US-0610424
95US-0009455
                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US15222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Sig_peptide
23..626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Cockrell G,
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                                      peanut allergens
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               WPI; 1998-377279/32
                                       Bower NI,
                                                                                           20-DEC-1996;
                                                                                                                                                                    WO9827805-A1
                                                                                                                                                                                                                                             Glycine max antimicrobial protein
                                                                 (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
                                                                                                                    22-DEC-1997;
                                                                                                                                           02-JUL-1998
                                                                                                                                                                                                                       antimicrobial protein; infestation; control.
                                                                                                                                                                                                                                                                         27-OCT-1998
                                                                                                                                                                                                                                                                                                                       W62838 standard; Protein; 605
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                                                                                                                                                                                                                                                                                                                                                                                                             PRQHQQQSPRSTKQQQP 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRG----PYNLFNKRPLYSNK 467
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                                        Goulter KC,
                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                    97WO-AU00874
                                       Green JL,
                                        Manners JM,
                                       Marcus
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                 Y40999 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 63-65; 96pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals
                                                                                                                                      591
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                                                                                                                                                                                                                                                           GRGGGK-----RHEEEEEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            llkvekeeceegeiprprprpqhperepqqpge-----keededeqprpipfprpq
                                                                                                                                   kgrk--gplssil
                                                                                                                                                              RSTKQQQPLVSIL 661
                                                                                                                                                                                                                                           ---glkeqqqeeqplevrkyraelseqdifvipagypvvv--natsnlnffaigin
                                                                                                                                                                                                                                                                                                itpeknpqlrdldiflsivdmnegalllphfnskaivilvinegdanielv------
                                                                                                                                                                                                                                                                                                                                                                    QR--EGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRFLYSNKYGQAYE
                                                                                                                                                                                                                                                                                                                                                                                                        laipvnkpgrfesfflssteaqqsylqgfsrnileasydtkfeeinkvlfsreegqqqge
                                                                                                                                                                                                                                                                                                                                                                                                                      NKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prqeeehegreegewpr----gfp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEQCOKHCORRETE-PRHMOTCOORCERRYEKEKRKOOKRYEEQQREDEEKYEERMKEED 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQRD----PQQQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aenngrnflagsgdnvisgipsgvgelafpgsagavekllkngresyfvdagpkkkeegn
                                                                                                                                                                                                                 AQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSP
                                                                                                                                                                                                                                                                                                                                                   qrlqesviveiskeqiralskraksss----rktissedkpfnlrsrdpiysnklgkffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fprpphqke----erneeedede-----eggreseesed------selr
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                                                                                                                                     601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%; Score 840.5; DB 19; 30.5%; Pred. No. 1.3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammalian
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Best Local S
Matches 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tertiary structure of peanut allergen Ara animal from allergic reaction - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1998;
11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 33A-B; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-551218/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sampson H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burks W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peanut; allergen; Ara H 1; IgE; immunoglobuli allergic reaction; soybean; beta-conglycinin.
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{\tt 309\ laipvnkpgrfesfflsstraqqsylqgfsrnilesaydtkfeeinkvlfsreegqqqge}
                                                                                                          305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LLFLLSLFLLSTTVSLAESEFDRQ--EYEECKRQCMQLETSGQMRRCVSQCDKRFEEDID 68
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                                                                                                                                                                                                                                                                                                   YEQCQKHCQRRETE-PRHMQTCQQRCERRYEKKKQQKRYEEQQREDEEKYEERMKEED 184
                                  FLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF------GQ 415
                                                                                        THLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAK 364
                                                                                                                                     rhknknpflfgsnrfetlfknqygrirvlqrfnqrspqlqnlrdyrilefnskpntlllp\\
                                                                                                                                                                                                                               NKRDPQQREYEDCRRCCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGE 244
                                                                                                                                                                                                                                                                              prqeeeheqreeqewpr-----keekrgekgseeededeegge---rgfp 154
                                                                                                                                                                                                                                                                                                                                                  llkvekeeckkgeiprprprpqhperepqqpge-----keededeqprpipfprpq 110
                                                                    nhadadylivilngtailslvnnddrdsyrlqsgdalrvpsgttyyvvnpdnnenlrlit 308
                                                                                                                                                          EEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLP 304
                                                                                                                                                                                                             fprpphqke-----erneeedede----eqqreseesed---
                                                                                                                                                                                                                                                                                                                                                                                    WSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQRD----PQQQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                     llllglvflasvsvsfgiaywekknpkhnkclqscnserdsyrnqacharc----n 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 23.5%; Score 831.5; Similarity 30.3%; Pred. No. 7.66 04; Conservative 145; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helm RM, Cockrell G, Bannon GA, Stanley JS, S, Compadre CM, Huang SK, Maleki SJ, Kopper RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0077763
99US-0077763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.6e-64;
nes 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protection of a host
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                                                                                                                                                                                                           ----selr 188
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                                                                                                         416 OR--EGVIIRASQEQIRELTRODSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYE
591 kgrk--gplssil 601
                                                       531
                                                                                                                                                                425 itpeknpqlrdldiflsivdmnegalllphfnskaivilvinegdanielv------
                                                                                                                                                                                                                    474 VKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHG
                                                     aenngrnflagsgdnvisgipsgvgelafpgsagavkkllkngrksyfvdagpkkkeegn
                          RSTKQQQPLVSIL 661
                                                                     AQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSP
                                                                                                                                                                  475
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